

APR 18 2003

TECH CENTER



1600

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/075,375E

DATE: 04/09/2003

TIME: 10:51:34

Input Set : A:\15619US03.txt

Output Set: N:\CRF4\04092003\I075375E.raw

3 <110> APPLICANT: Yamamoto, Harry Y
4 Bugos, Robert C.
5 Rockholm, David C
7 <120> TITLE OF INVENTION: PLANT VDE GENES AND METHODS RELATED THERETO
9 <130> FILE REFERENCE: 15619/03/US
11 <140> CURRENT APPLICATION NUMBER: US 09/075,375E
12 <141> CURRENT FILING DATE: 1998-05-07
14 <150> PRIOR APPLICATION NUMBER: US08/747,574
15 <151> PRIOR FILING DATE: 1996-11-07
17 <150> PRIOR APPLICATION NUMBER: PCT/US96/18291
18 <151> PRIOR FILING DATE: 1996-11-07
20 <150> PRIOR APPLICATION NUMBER: US 60/023,502
21 <151> PRIOR FILING DATE: 1996-08-06
23 <150> PRIOR APPLICATION NUMBER: US 60/006,315
24 <151> PRIOR FILING DATE: 1995-11-07
26 <160> NUMBER OF SEQ ID NOS: 9
28 <170> SOFTWARE: PatentIn version 3.2
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 1981
32 <212> TYPE: DNA
33 <213> ORGANISM: Lactuca sativa
35 <400> SEQUENCE: 1
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38 aatttccctt gtacaatttt ccaatttctt cctccgccac accatatata tactgtacgc 120
40 cacttcgaac gctacaatgt ttgaaaaaag acgcagattt tacaagacg gagaagataa 180
42 taagcttcaa gtactccgat cgtcagggtg cctttggaag ccaacaaact ggctatggct 240
44 ctttctcttc aactgtatt tctctgcaaa gaggaagccc tcaatttata tgcaagatca 300
46 ccatgtaatg aaaggtttca caggagtga caacctccta ccaacataat catgatgaaa 360
48 attcgatcca acaatggata ttttaattct ttccggttgt ttacatctta taagacaagt 420
50 tctttctcag attctagcca ttgcaaggat aaatctcaga tatgcagcat cgatacaagt 480
52 tttgaggaaa tacaagatt tgatctcaaa aggggcata ctttgattct tgaaaagcaa 540
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56 gttgatgccg ttgatgctct taaaacttgt gcttggtttac tcaaagaatg caggattgag 660
58 cttgcaaaat gtatagcaaa cccatcttgt gcggcacacg ttgctgtct acagacttgc 720
60 aacaatcgtc ctgacgagac cgaatgtcag ataaaatgtg gtgacttggt cgaaaacagt 780
62 gtggtggacc aattcaacga gtgtgcggtt tcccgaaaga aatgtgtgcc ccggaaatcg 840
64 gatgtgggtg aattcccggt tccggtatcg aatgcagtgg ttcaaaattt taacatgaaa 900
66 gactttagtg ggaagtggta tataacaagt ggtttaaatc ctacatttga tgcatttgat 960
68 tgtcaacttc atgagtttca tatggaaaat gataaacttg ttgggaactt aacatggcgc 1020
70 ataaaaactt tggatgggtg tttctttact cgatctgctg tgcaaacatt tgttcaagat 1080
72 ccagatcttc ctggagcact ttataatcat gacaatgagt ttcttacta ccaagatgac 1140
74 tggtagatat tatcttccca aatcgaaaac aaaccgatg attacatatt cgtatactac 1200
76 cgaggtcgaa acgacgcgtg ggatggatac ggtgggtccg tgatctacac ccgaagcccg 1260

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80 tttacaatt tcataacaac cgacaatagt tgtgggcctg agcctccatt ggtggaaagg 1380
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84 gaagaggttg aaaaagaggt ggagaagggt agagatactg agatgacttt gtttcagagg 1500
86 ttgcttgaag ggtttaagga gttgcaacaa gatgaagaga attttgtgag ggagttgagt 1560
88 aaagaagaga aggaaattct gaatgaactt caaatggaag cgactgaagt tgaaaagctt 1620
90 tttgggcgcg cgttaccgat taggaaactt agataaattt cgatgattga ttcagacaat 1680
92 atatatagtc atatggatta tgtagatact agagaaaacc caaaaaaact tttgtatacg 1740
94 tgataaacgt gtttgtgatt tgtttatttg cttaaaattg tagaatagct tttttaattc 1800
96 tttacaaaaa aattgattgt ctattggtag ccaagagggt cagcaaaaga ctgaaagggt 1860
98 cttgccggtt tgcggggttag gccaaatttt ttggggcggg atcgggtctg atcgggtttt 1920
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102 a 1981
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106 <211> LENGTH: 1412
107 <212> TYPE: PRT
108 <213> ORGANISM: Lactuca sativa
110 <400> SEQUENCE: 2
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116 Asn Leu Tyr Ala Arg Ser Pro Cys Asn Glu Arg Phe His Arg Ser Gly
117 20 25 30
120 Gln Pro Pro Thr Asn Ile Ile Met Lys Ile Arg Ser Asn Asn Gly
121 35 40 45
124 Tyr Phe Asn Ser Phe Arg Leu Phe Thr Ser Tyr Lys Thr Ser Ser Phe
125 50 55 60
128 Ser Asp Ser Ser His Cys Lys Asp Lys Ser Gln Ile Cys Ser Ile Asp
129 65 70 75 80
132 Thr Ser Phe Glu Glu Ile Gln Arg Phe Asp Leu Lys Arg Gly Met Thr
133 85 90 95
136 Leu Ile Leu Glu Lys Gln Trp Arg Gln Phe Ile Gln Leu Ala Ile Val
137 100 105 110
140 Leu Val Cys Thr Phe Val Ile Val Pro Arg Val Asp Ala Val Asp Ala
141 115 120 125
144 Leu Lys Thr Cys Ala Cys Leu Leu Lys Glu Cys Arg Ile Glu Leu Ala
145 130 135 140
148 Lys Cys Ile Ala Asn Pro Ser Cys Ala Ala Asn Val Ala Cys Leu Gln
149 145 150 155 160
152 Thr Cys Asn Asn Arg Pro Asp Glu Thr Glu Cys Gln Ile Lys Cys Gly
153 165 170 175
156 Asp Leu Phe Glu Asn Ser Val Val Asp Gln Phe Asn Glu Cys Ala Val
157 180 185 190
160 Ser Arg Lys Lys Cys Val Pro Arg Lys Ser Asp Val Gly Glu Phe Pro
161 195 200 205
164 Val Pro Asp Arg Asn Ala Val Val Gln Asn Phe Asn Met Lys Asp Phe
165 210 215 220
168 Ser Gly Lys Trp Tyr Ile Thr Ser Gly Leu Asn Pro Thr Phe Asp Ala
169 225 230 235 240
172 Phe Asp Cys Gln Leu His Glu Phe His Met Glu Asn Asp Lys Leu Val

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173          245          250          255
176 Gly Asn Leu Thr Trp Arg Ile Lys Thr Leu Asp Gly Gly Phe Phe Thr
177          260          265          270
180 Arg Ser Ala Val Gln Thr Phe Val Gln Asp Pro Asp Leu Pro Gly Ala
181          275          280          285
184 Leu Tyr Asn His Asp Asn Glu Phe Leu His Tyr Gln Asp Asp Trp Tyr
185          290          295          300
188 Ile Leu Ser Ser Gln Ile Glu Asn Lys Pro Asp Asp Tyr Ile Phe Val
189 305          310          315          320
192 Tyr Tyr Arg Gly Arg Asn Asp Ala Trp Asp Gly Tyr Gly Gly Ser Val
193          325          330          335
196 Ile Tyr Thr Arg Ser Pro Thr Leu Pro Glu Ser Ile Ile Pro Asn Leu
197          340          345          350
200 Gln Lys Ala Ala Lys Ser Val Gly Arg Asp Phe Asn Asn Phe Ile Thr
201          355          360          365
204 Thr Asp Asn Ser Cys Gly Pro Glu Pro Pro Leu Val Glu Arg Leu Glu
205          370          375          380
208 Lys Thr Ala Glu Glu Gly Glu Lys Leu Leu Ile Lys Glu Ala Val Glu
209 385          390          395          400
212 Ile Glu Glu Glu Val Glu Lys Glu Val Glu Lys Val Arg Asp Thr Glu
213          405          410          415
216 Met Thr Leu Phe Gln Arg Leu Leu Glu Gly Phe Lys Glu Leu Gln Gln
217          420          425          430
220 Asp Glu Glu Asn Phe Val Arg Glu Leu Ser Lys Glu Glu Lys Glu Ile
221          435          440          445
224 Leu Asn Glu Leu Gln Met Glu Ala Thr Glu Val Glu Lys Leu Phe Gly
225          450          455          460
228 Arg Ala Leu Pro Ile Arg Lys Leu Arg Met Ala Leu Ala Pro His Ser
229 465          470          475          480
232 Asn Phe Leu Ala Asn His Glu Thr Ile Lys Tyr Tyr Val Gly Ser Lys
233          485          490          495
236 Leu Pro Gly His Lys Arg Phe Ser Trp Gly Trp Glu Asp Tyr Phe Gly
237          500          505          510
240 Ser Ile Val Val Ala Lys Ile Cys Ser Ser Arg Arg Ile Pro Arg Tyr
241          515          520          525
244 Phe Arg Lys Ser Pro Arg Ile Cys Cys Gly Leu Asp Ser Arg Gly Leu
245          530          535          540
248 Gln Leu Phe Ser His Gly Lys His Asn Leu Ser Pro Ala His Ser Ile
249 545          550          555          560
252 Asn Gln Asn Val Pro Lys Gly Asn Ser Gly Cys Lys Phe Pro Lys Asp
253          565          570          575
256 Val Ala Leu Met Val Trp Glu Lys Trp Gly Gln Phe Ala Lys Thr Ala
257          580          585          590
260 Ile Val Ala Ile Phe Ile Leu Ser Val Ala Ser Lys Ala Asp Ala Val
261          595          600          605
264 Asp Ala Leu Lys Thr Cys Thr Cys Leu Leu Lys Glu Cys Arg Leu Glu
265          610          615          620
268 Leu Ala Lys Cys Ile Ser Asn Pro Ala Cys Ala Ala Asn Val Ala Cys
269 625          630          635          640

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272 Leu Gln Thr Cys Asn Asn Arg Pro Asp Glu Thr Glu Cys Gln Ile Lys
273           645           650           655
276 Cys Gly Asp Leu Phe Glu Asn Ser Val Val Asp Glu Phe Asn Glu Cys
277           660           665           670
280 Ala Val Ser Arg Lys Lys Cys Val Pro Arg Lys Ser Asp Val Gly Asp
281           675           680           685
284 Phe Pro Val Pro Asp Pro Ser Val Leu Val Gln Lys Phe Asp Met Lys
285           690           695           700
288 Asp Phe Ser Gly Lys Trp Phe Ile Thr Arg Gly Leu Asn Pro Thr Phe
289 705           710           715           720
292 Asp Ala Phe Asp Cys Gln Leu His Glu Phe His Thr Glu Glu Asn Lys
293           725           730           735
296 Leu Val Gly Asn Leu Ser Trp Arg Ile Arg Thr Pro Asp Gly Gly Phe
297           740           745           750
300 Phe Thr Arg Ser Ala Val Gln Lys Phe Val Gln Asp Pro Lys Tyr Pro
301           755           760           765
304 Gly Ile Leu Tyr Asn His Asp Asn Glu Tyr Leu Leu Tyr Gln Asp Asp
305           770           775           780
308 Trp Tyr Ile Leu Ser Ser Lys Val Glu Asn Ser Pro Glu Asp Tyr Ile
309 785           790           795           800
312 Phe Val Tyr Tyr Lys Gly Arg Asn Asp Ala Trp Asp Gly Tyr Gly Gly
313           805           810           815
316 Ser Val Leu Tyr Thr Arg Ser Ala Val Leu Pro Glu Ser Ile Ile Pro
317           820           825           830
320 Glu Leu Gln Thr Ala Ala Gln Lys Val Gly Arg Asp Phe Asn Thr Phe
321           835           840           845
324 Ile Lys Thr Asp Asn Thr Cys Gly Pro Glu Pro Pro Leu Val Glu Arg
325           850           855           860
328 Leu Glu Lys Lys Val Glu Glu Gly Glu Arg Thr Ile Ile Lys Glu Val
329 865           870           875           880
332 Glu Glu Ile Glu Glu Glu Val Glu Lys Val Arg Asp Lys Glu Val Thr
333           885           890           895
336 Leu Phe Ser Lys Leu Phe Glu Gly Phe Lys Glu Leu Gln Arg Asp Glu
337           900           905           910
340 Glu Asn Phe Leu Arg Glu Leu Ser Lys Glu Glu Met Asp Val Leu Asp
341           915           920           925
344 Gly Leu Lys Met Glu Ala Thr Glu Val Glu Lys Leu Phe Gly Arg Ala
345           930           935           940
348 Leu Pro Ile Arg Lys Leu Met Ala Val Ala Thr His Cys Phe Thr Ser
349 945           950           955           960
352 Pro Cys His Asp Arg Ile Arg Phe Phe Ser Ser Asp Asp Gly Ile Gly
353           965           970           975
356 Arg Leu Gly Ile Thr Arg Lys Arg Ile Asn Gly Thr Phe Leu Leu Lys
357           980           985           990
360 Ile Leu Pro Pro Ile Gln Ser Ala Asp Leu Arg Thr Thr Gly Gly Arg
361           995           1000          1005
364 Ser Ser Arg Pro Leu Ser Ala Phe Arg Ser Gly Phe Ser Lys Gly
365           1010          1015          1020
368 Ile Phe Asp Ile Val Pro Leu Pro Ser Lys Asn Glu Leu Lys Glu

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369	1025	1030	1035
372	Leu Thr Ala Pro Leu Leu Leu	Lys Leu Val Gly Val	Leu Ala Cys
373	1040	1045	1050
376	Ala Phe Leu Ile Val Pro Ser	Ala Asp Ala Val Asp	Ala Leu Lys
377	1055	1060	1065
380	Thr Cys Ala Cys Leu Leu Lys	Gly Cys Arg Ile Glu	Leu Ala Lys
381	1070	1075	1080
384	Cys Ile Ala Asn Pro Ala Cys	Ala Ala Asn Val Ala	Cys Leu Gln
385	1085	1090	1095
388	Thr Cys Asn Asn Arg Pro Asp	Glu Thr Glu Cys Gln	Ile Lys Cys
389	1100	1105	1110
392	Gly Asp Leu Phe Glu Asn Ser	Val Val Asp Glu Phe	Asn Glu Cys
393	1115	1120	1125
396	Ala Val Ser Arg Lys Lys Cys	Val Pro Arg Lys Ser	Asp Leu Gly
397	1130	1135	1140
400	Glu Phe Pro Ala Pro Asp Pro	Ser Val Leu Val Gln	Asn Phe Asn
401	1145	1150	1155
404	Ile Ser Asp Phe Asn Gly Lys	Trp Tyr Ile Thr Ser	Gly Leu Asn
405	1160	1165	1170
408	Pro Thr Phe Asp Ala Phe Asp	Cys Gln Leu His Glu	Phe His Thr
409	1175	1180	1185
412	Glu Gly Asp Asn Lys Leu Val	Gly Asn Ile Ser Trp	Arg Ile Lys
413	1190	1195	1200
416	Thr Leu Asp Ser Gly Phe Phe	Thr Arg Ser Ala Val	Gln Lys Phe
417	1205	1210	1215
420	Val Gln Asp Pro Asn Gln Pro	Gly Val Leu Tyr Asn	His Asp Asn
421	1220	1225	1230
424	Glu Tyr Leu His Tyr Gln Asp	Asp Trp Tyr Ile Leu	Ser Ser Lys
425	1235	1240	1245
428	Ile Glu Asn Lys Pro Glu Asp	Tyr Ile Phe Val Tyr	Tyr Arg Gly
429	1250	1255	1260
432	Arg Asn Asp Ala Trp Asp Gly	Tyr Gly Gly Ala Val	Val Tyr Thr
433	1265	1270	1275
436	Arg Ser Ser Val Leu Pro Asn	Ser Ile Ile Pro Glu	Leu Glu Lys
437	1280	1285	1290
440	Ala Ala Lys Ser Ile Gly Arg	Asp Phe Ser Thr Phe	Ile Arg Thr
441	1295	1300	1305
444	Asp Asn Thr Cys Gly Pro Glu	Pro Ala Leu Val Glu	Arg Ile Glu
445	1310	1315	1320
448	Lys Thr Val Glu Glu Gly Glu	Arg Ile Ile Val Lys	Glu Val Glu
449	1325	1330	1335
452	Glu Ile Glu Glu Glu Val Glu	Lys Glu Val Glu Lys	Val Gly Arg
453	1340	1345	1350
456	Thr Glu Met Thr Leu Phe Gln	Arg Leu Ala Glu Gly	Phe Asn Glu
457	1355	1360	1365
460	Leu Lys Gln Asp Glu Glu Asn	Phe Val Arg Glu Leu	Ser Lys Glu
461	1370	1375	1380
464	Glu Met Glu Phe Leu Asp Glu	Ile Lys Met Glu Ala	Ser Glu Val
465	1385	1390	1395

RAW SEQUENCE LISTING ERROR SUMMARY
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:7,8,9

VERIFICATION SUMMARY

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